

FIGURE 1

66340-2030660



FIGURE 2

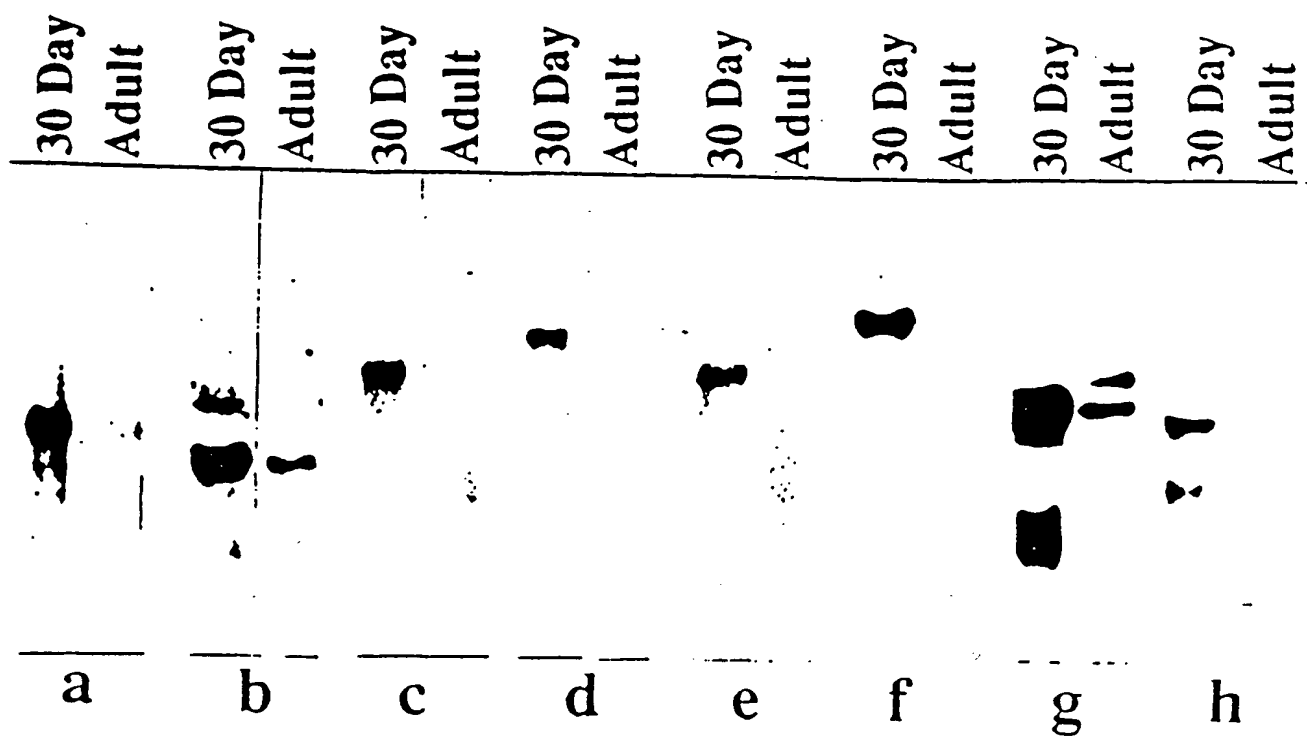


FIGURE 3

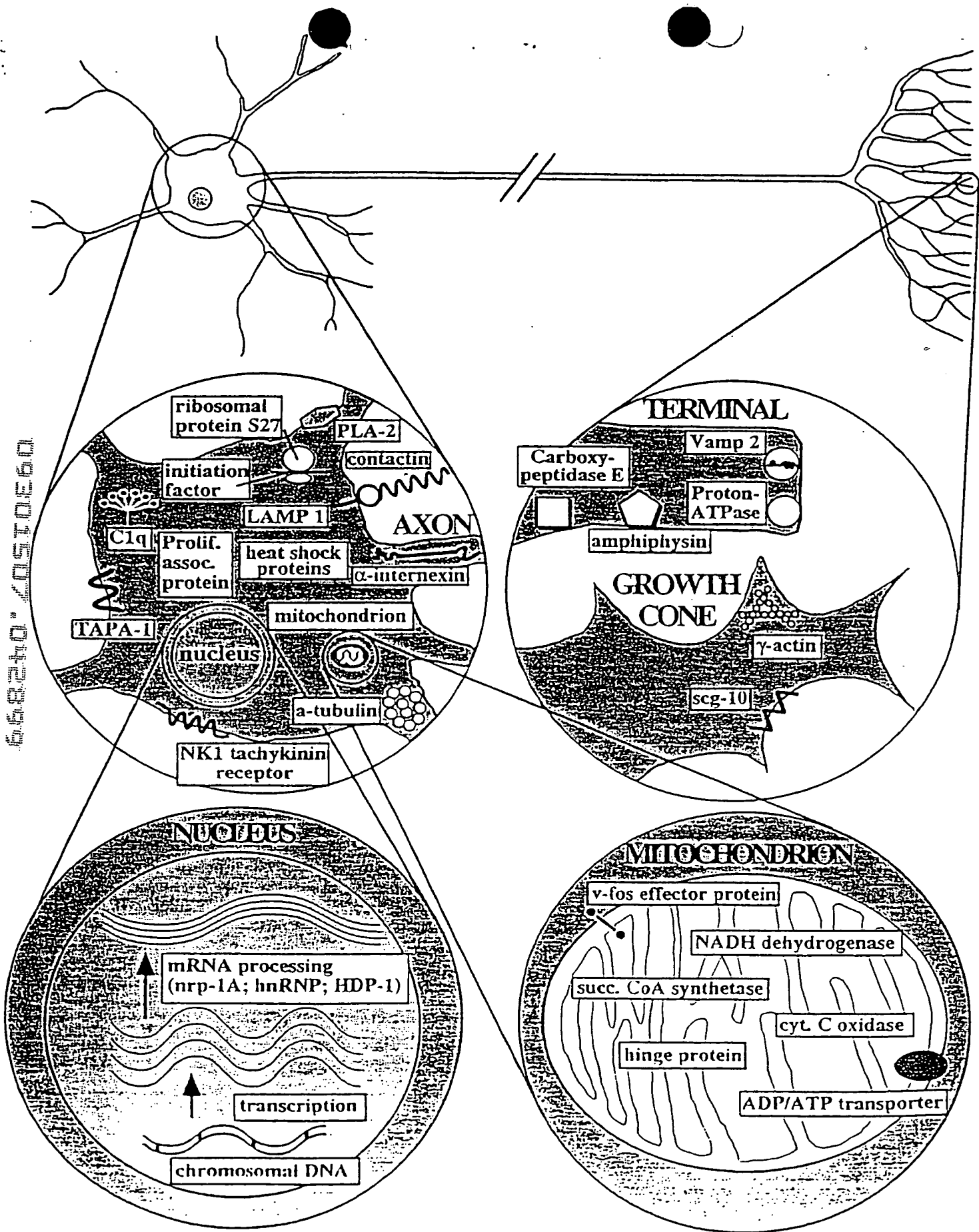


FIGURE 4

663240-0570560

SEQ ID. NO.: 1

pKVC43:

CCTGGCTGCCTGTGCCTCAACCCCACTCCCAGGGAGACCAAAAGCCTTCATACATCTGAA AT

SEQ ID. NO.: 2

pKVC2B:

GCGACGGACGAGATGTCTTCGGTGTCTTGCCTTCGCTACCAGGTCAAAATGCAAATCTTCGTGAAAAC
CCTGACgGGCAAGACCATCACCC

SEQ ID. NO.: 3

pKVC15:

TTTTTTTTTAATTGAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAACACCGTTTCGATT
CCTTCCTTTCTTATTTTAATAGTACGTtAAGTTGGCTCTTCAAAT

SEQ. ID. NO.: 4

>pKVC24BR

poly(T)ATCCATACTTGCTATTTATTTAGGCTTCTAGTTTGGAAACAAAAGGNCAAGAGTTAAAAAAT
GCCAACATTTCAAGGACCCTTGTT

SEQ ID. NO.: 5

pKVC26B:

CTTCCCCCACTCATCCCTGCTCTGGTCCCTTGTgCCCCCTTGGCCCTTTACCCCAAGCACCACCCACAG
ACTGGGGACCAGCCCCCTCTCCTGCCTATGTCTCgCCCCAAAT

SEQ ID. NO.: 6

pKVC50B:

CCTTCCCTTCCTTACTTTAATAGTTTCGGTAGTACGGANGTTAAATCTTCAGGTGGTGGTACGCAGCCG
GGCAACCATGCAATGGATTNAAGGTNGGTAATGGTACAATTGGCCTATGCCCACTTT

SEQ ID. NO.: 7

pKVC85B:

CTTTAGAGCGCACTCAGGGGCACTTGNAAGGGCTTCTCACGAGCGTGGCTGTGGCCATCTGTGGAAAGA
GCTTCTCGCAGTGNTCGGTNGNNTTATCCCCACGCCNTAGNGCACTACTC

SEQ ID. NO.: 8

pKVC100:

TTAGTTTCACATTCAAGGGGCTTATGAAGAGATGCAAGTCAGGATACATAGGCTTGATTC
TTGGCAGCTTAaTGAGTaTTCACtGAGGCACTtG

SEQ ID. NO.: 9

pKVC94B:

CCGCCTGATATAGACACTTCGTAGAGCGTAGTTTGACTATTCCTATACGTTTCTATTTATTGATGAGGA
TCCTAAA

FIGURE 5A

SEQ ID. NO.: 10

pKVC90B:

TTTATTATGCACACGTTGTTCAAATAAACCAGTGTGGGATGTTAAGACTATCAATTAATGGTGGGATTA
TGTTTGGCATTATTTATTNNTTATAAATATATATTTTTCTGAATGTGTCCTGAGNTCCAAAGAGGTTGGG
GGNGGGGGNG

SEQ ID. NO.: 11

pKVC91B:

TTTCCTTGGGTTGCTGGTTGGATTAATCTTTAATAACAATATATAGAATTGTAGACTGATGTTTTAGTG
TTTTTCCAACACACAAACATAAAAAATAAAACAAGTCGGACCGCTACTTCTGTGTAAATCAAGATCNTT
GGGGAA

SEQ ID. NO.: 12

pKVC101B:

CCTGGCCAGCGGGCAGGGCCACGAAGGCAAGATCGGTCGTTGTGCTTGTGTTTTCCAAGGAGACGANCC
NATNANCTGTAAATATGTACACGTNTCTGTCTGTGTGTCCTTCGNGGNAGG
ATGGTCGGNTCTATTAAA

SEQ ID. NO.: 13

pKVC103fB:

CCAAAATATATTTGGGCCAAATGTTCCGAGGATGAGTCAGGCTGTCCTTCGCGCGGGCGAGACGAAGCT
TCACACGGGACAAGATGGGATGGGTTGGAGGAATGGATGGTCCCCCAAACA
ATGGGCTTANAANAATTAT

SEQ ID. NO.: 14

pKVC105:

TTTACTGACAAGCATGGGGAAGTGTGCCAGCTGGCTGGAAGCTGGCAGTGATACCATCAAGCCTGATG
TCcAGAAGAGCAAAGAATATTTCTCTAAGCAGAAGTGAGCGCTAGGCCTTTT

SEQ ID. NO.: 15

pKVC107:

CGGCTTCcTGGGCTTTATCGTATGAGCCCATCACATGTTTACTGTAGGAATGGATGTAGACACACGAGC
ATACTTTACATCAGCCACTATAATTATTGCCATTCCcTACCGGGGTGAAAGT ATTAGTTGACT

SEQ ID. NO.: 16

pKVC1B:

GGAGCTTGAAGAAGAAGTTTTTTACCACCGTCTTTTTCTACTTTATACAGAAGTAGATATTCCTGCGAA
GAAGAATAATTTGGGGTAATATGCAAGCTAGTAGATGTGGCACAGCAAATC ATATAATAAA

SEQ ID. NO.: 17

pKVC5B:

ACCCACCCAGAGCCTGGAATCAGGATCCAGGGTCTAGCCAGCCTGGGGTCCAGAACCCAGAATCCAG
CCTGTCTGAGCTGGACCTAGCAGCCAGAGTCTAGCCAGCCTCGCTCCAAGAGGGGCTCTGGTGGCCTA
GGTAGACAGGCCTGgTGGGGATCAATGAGTTGGTGTAGGGCCAGGGCACCTCGACTCTGCTCCATAC
TG

FIGURE 5B

CACCTTCCTGAAACACCTGTGGCTTTGACTTTGTTATTGATCCAGATTATTCTCCTTGCATTGGGGAAA
ATATCTTTCATATTTCACTGTAAGGGATGTTTTGCCGAGAGTAAGTTAATGTCAAGACAACTGCCAAT
ACAAGAGCCCAATGATATTAATTACATGAGAAAAaGTA ACTA ATACATCC

GAGAAAGAAAGAGATGTTTTATTAGCATTTGTTACAGCAACGgTGACGTGAAGGGTCGTCCGTGCACAG
CCACCCGAGCGGCAAGGCGTAGGCCAGAGCTGACACCCAGTATTTACACGAGTGCAGAACAGGATCACC
CCGAACCTCAAACAGAAGACTGAAAGTCACTTTACAAAAAGGTAAATAAAAA

GCTACGGTCGACATCACCATCTTTATCCCTTCCAGCCCTTTGCTGGGTCGCGGGCCTTGGGAAGATGCC
AAAGAGCCGAGCAGTGGTGGTGGCCAGCGGCAGAGTGTCCCTGCTTGGGCCAGGAAAGCTTTACCTTC
TCTGAGCGCCTCTGCCTGAGAGATCGATGGTCTGTGGCTCTA GGAGACCACGTCTTGGAGTG

poly(T)CCTTCTTTATTGAATGACTTTCAAGAgGTAATTACAGTTGAAGGTGACAAGTTAGAAAGGAG
AGGTGCCACTGAAGGCATAAGGCTGCTTGTAGACCCGGCTCTAGACAAGTGGCAGGAGAAGAAAGAGGG
TAAAAAAGGCATGAGCGTGCAGCCACGGGGCA

GGCAGCACTCCTATTA^{AA}ACTGGAACCTACTGAGGTTTCCTCGTGTAATTAGGGAACAGAGAAACACgt
tCCACGAGGGAGCCTCCAGGTCTAATTACCTGCAACCTCGCTGTACCTTGCTGGCGAGGAGGGAGCCAC
CAATAGCAATTACTAACGAATGGCTGAATTCCTTATAAGACCTAGGGAACCTGATGGGAAACTGAATT
GCTAA

TTTTTTTTTTTAAATTTTTTAAACGTTTATTTATTTTGGAGACAGAGAGAGACAGAGCATGAACGGG
GGAGGGGCAGAGAGAGAGGGAGACACAGAATCGGAAGCATGCTCCAGGCTCTGAGCCCATCAGCCCAGA
GCCCAGCGCGGGCTCGAACTCACGGACTGTGAGATCGTGACCTGAGCCGAAGTCAGACGCCCAACCAAC
TGAGCCACCCAGGCGCACCATC

CCAGGTGACAGGGAGCCTGCAGGGAGGGTCTGGGTGTTCCAGGAGCCAGGGGAAGTGGGAATGGTGCA
GGCAGTATTGGAAGGAAGGCCAGTCAGTGGGACTGGCAGCTCAGACAGGCAATATGGGGAAGCATTGGA
GCTTGAGTCTCCACTCTGGGGTTAGGGGTTTGCACACTCAGCAATAAATAACTGTGTACACCAAATC
CTAAATATATCACTACAAA

FIGURE 5C

SEQ. ID. NO.: 25

>pKVC79R

poly(T)GTGTTAAGTGGTCTTTATTGGGGTGTCACATTAGGTTATCTTCTTCATTATCAGTTCTTCAG
TTAATTGTACAAGTATGATAAGTTATTTTATATCTGACGTGGGAATTTAAATGTAAAATAAATACAAAA
TACATCTGTGGTTTAATGAACACTCAATGAAGAC

SEQ ID. NO.: 26

pKVC30:

ACAACAACGTGTGCAGGTGCTTTTGTGTGGAGTGTGTGGATCTGTTGGTGGGGCCGGGGGGCCAGGAC
TCAAGGAGGACCCCTGGAACGTGCTACATGTGCGGGCACAAGGGCACCTACGGGCTGCTGCGGCGGCGGG
ACGACTGGCCCTCGCGGCTGCAGATGTTCTTTGCCAATAACCACGACCAGGAGTTTGACCCTCCGAAGT
TTACCCA

SEQ. ID. NO.: 27

>pKVC7R

poly(T)ACACAGAACAAGAAATTTTATTATCTCGAATGCTGGTGCATAAgCAATAACAAGCTCATCAA
TTAGAGGAGGAGACAGAGGGAACTTCAGATACTGATGAGGATTTCTGGGCAGGTTTAAACCTTTAA
GATTGAGGCCATAATTGTTcAGTCTTTTTTT

SEQ ID. NO.: 28

pKVC32B:

CCTTGCCAAGGCCGAGGCTCCACAGGAATCAGAGTTGGGACGACNNNGAAGGAAGCGTTTGGCTTCAC
ATTCTAGAGAAAGAAGACCCTACTGGGCTGCAGACCCCTCCAGGGCTGTAGGAAAGCTGCTGGACCTCT
TCTGCTTCTCCCCAACCCTCTGCCACTCTGCCAGTTACCAG TCACCAG

SEQ. ID NO.: 29

>pKVC45BR

TTCAGAATACTGTTTTTTTTTTTTTTTAAATTTGTTTTGGTTTGTGTTTTGTTTTAATTTAAAGAAAGGT
ATTTTGCTTGAGGAAAAATACTCCAGATTCATTTAATGAGAATCTTTGAAATGTATTTATCTTTAGG
GCATTTGGGGCAACTTTAATGCCTGTTGGCCTCCGGCCTCCTGGAAATAAAAGGTCCAACGG

SEQ ID. NO.: 30

pKVC34B:

CCTGCCCCACGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGACGGACTACCTCATGAAGATCCT
CACAGAGCGCGGCTACAGCTTCACCACCACCGCCGAGCGGAAATTGTGCGTGACATCAAGGAGAAGCTC
TGCTACGTGGCCTTGGACTTCGAGCAGGAGATGGCCACCGCCGCGTCTCGTCCTCCTGGAGAAGAGCT
ACGAGCTGCCCCGAC

SEQ. ID. NO.: 31

>pKVC89BF

ATTGTGATAGAAGACCACGGTGGGTTCANCAANGTTGAAGNAGTTCCGCNTTTCCCTCCGGGGGAAAG
GTTGTGATGTCTNTTGGTNNTAAGTANTACCCATNCATTGTTGACAAGGNTCANTCCCGAAGGGTCA
TTCTTGAGTAGTAGACCAATATTNTAAAAATAATTTNAATCCTT

FIGURE 5D

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SEQ ID. NO.: 32

pKVC34:

AATTGAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCCTTT
CTTATTTTAATAGTACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATCCATGCAATCATT
CAAGATTAGTTGTGGTTAATTCTACTATGGCCACTTCTCGCTTGGATGCGAAAGCTTCTCACACTATGA
AAA

SEQ ID. NO.: 33

pKVC36B:

ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTGAAGGCTGCTTAGGCGCATTGT
AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAAATGTAGTGCTCGAAACACATTCTGCTT
TAAAAGGTTGTAACAAATACAAACAAATTTAAAAAAGCTCT CGAAAA

SEQ ID. NO.: 34

pKVC43rB:

CTGGAGCGCAAGTACTCCGTGTGGATCGGTGGCTCCATCCCGGGCTTGGTGTCCACCTTCCACAAGTG
TTGATCACACAAGCCGGAGTACGCGCGCGGTTTCGGCCCCCTTCATAGGCCACCGCAAAAACCTTTTAGGC
GGGCTCTTACNTTAGAGGCGGTACACACCTTCTTG

SEQ ID. NO.: 35

pKVC73:

TGGGCATCAAATGAAAGAGATACTTGCAAAGGCTCTTGAGGGGCAGGGAAAGGAAAGGAGGACTGTCTG
CTTTGGACCCTAACTGGACAGGGACTAGGTATTTTTGATGTTTATAAGTTGCTCTAAGTTCAT
TTGAGTAGCAGACCTGACAAGCATTTGAGGTCAAACCCTACCATGTGTAAAAAAAAA

SEQ ID. NO.: 36

pKVC79B:

GTCTTGATACAAAGCTTCTGTGCTAATCCAGACTATTTAGGCAGGGGCAATAGGGTGTAATGTATCT
GCTCTCTTCAAACGCGGCTAANGNTCTAGTCCATGTCCNCCNNGCAACCNNCAANATCCCACNAGGGG
GNAGNTCG

SEQ ID. NO.: 37

pKVC81B:

CCCAGGTGAACAGGAACAGGTTTTCTATAAAAAACAACAAAAATCCTTGCCATTCATTTCTTACTT
GNATGTGGAAAAATAGATCCGCCTTTATTGNTGAATAGCCTTAAACTTTTGGAGAATATTCCTTAGNA
AATTAGGGGGGGNGGGGC

SEQ ID. NO.: 38

pKVC83B:

CATCTAGATANTCTTGGNGATTGGGGCCTCTAGNTGATTGCTCGAGCGGCCGCCAGTGTGTTTTAAAGA
CTGGCTCAGGGCCTGTGCGAGGTGCTGCTGGTGGTGACCAAGGAGGTGGAGGAAAAGGGCTGCTGGNCT
GCGGNACAGTACTGACCCCGCGGAGGTAGTAGCAACCAGGTCCACCGTACCCCTGCGAGTCCCCCGCTG
CCAATCCCC

FIGURE 5E

SEQ ID. NO.: 39

pKVC87B:

CCACCAAGAAGCTGGACCTGTGGATGCTGCCTGAGACACTCATTATCCACCTGAAGCGCTTCTCTTACA
CCAAGTTCTCCCGCGAGAAGCTGGATACCCCTTGTGGAGTTTCCCATCCGGGACCTGGAACCTCTCCGAG
TTTGGCATCAAGTCCGTAGGAACGAGTCGGCTCCGGAGCTGTACAAATACGCATCTCATCGNGGGNTNC
CATCNCATTNATGGGGG

SEQ ID. NO.: 40

pKVC104fB:

GGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGGCGCCAGTGTGCTCTAAAGCCAAAATATATTTGA
GCCAAATGTTCCGAGGATGAGTCAGGCTGTCTTCGGGGGCAGNAAAGGCTTCACACGGGACAAGTGGAT
GGNTTGGAGGAATGNATGNTCCGCAACCATGGGCT

SEQ ID. NO.: 41

pKVC104:

CTGACTGGCCCAGAATTTTTGAATACTGGAGGCAGTCTCATTGGCCTCCCTCATTAGACTCCAGGATTC
GGTCCAGCCCAGAGCACTGTGGGCTCCTACCAGTCCAAAAGTCTAGGACCGCTTGCAGACCCAGGAAA
GGAATTTTCTAGTGTTCTACAAAGGCCAATAGAGAGGGTGGGAGTGGGTGGGGTGAGGACCGGTGGCGA
GAGGGG

SEQ ID. NO.: 42

pKVC109B:

GCCAGATTTACATAAGAACATGCTTAACAGACGATCTTTTAGCTGACGTCTTACCAGNAATCGCCCAAG
TCCGCACGGTAAGTAAAGAGGAGGCCCGCCAGGTGAGAGTTTGCTTAGCAATAGGGTCAGGTCACTAAA
ACTGTAAATCCATTGCGAGAGGGGGACGCCTCCGCTCAAGCT TGGCTGGGCTTCGGC

SEQ ID. NO.: 43

pKVC89B:

GTCAAAGAGACCAAATCCCATATCCTCATCTGATTCTCCGACTCTTCCTTTGCTTCAACCTTGGCTGG
GGCTGCAGCAGCAGCAGGTGCAGCAGTGGTGGCAGCGGCCACGGGGCAGCAGCCACAAATGCAGATGG
GATCAGCCAAGAAGGCCTTGGACCTTTTCAGGCAAGTGGGGAAGGTATAATCAGGTCTCCACAGGACAA
AGGCCAGGACCCGCTTATTTTCCATTGGATGGATAGGAATGGGGGGCACTGNATGCAAACAGGNCGGGG
TTNACCCTTTCTTGNAGGACCATT
TCA

SEQ ID. NO.: 44

pKVC115:

GCGCAGGCACAGCTGGTGAGGGGCGAGGCCGAGACGCCAAGGTGGCCACCATGGTCCGGAGTGCCTGC
AGGTAGTGGGCTTCGTACGAGCTTCGTGGGTGGATCGGCATCATCGTCACCACGTCCACCAACGACT
GGGTGGTGACCTGCGGCTACACCATCCCCACCTGCCGCAAGCTGGACGAAGTGGGCTCCAAGGGGCTGT
GGGCAGACTC

SEQ ID. NO.: 45

FIGURE 5F

pKVC20fB:

CAAACCCATGCATACCACATAGTCAACCCTAGCCCATGGCCACTTACAGGAGCCCTTtCAGCCCTCTTA
ATAACCTCAGGCCTGGCTATATGATTCCACTACAACCTCAACACTGCTGTTAACCCTTGGAATAACTACC
AACCTACTAACTATATATCAATGATGACGAGACATTATCcgAGAAAGCACATTCCAAGGCCATCATACA
CCTATCGTTCAAAAAGG

SEQ ID. NO.: 46

pKVC7B:

GCGCCCGCCGCGTCGCGCCGCCTACCGCCGTACCACCCGCCGCCTCCTCTGCAACCTCAGCCCACCGG
GGCACCCGGCCAGGTCACTGGCGGCCAGGCGCAGCTCCTGGAGGAGAATGACCAGCTCATCCGCTGT
ATCGTGGAGTATCAGAACAAGGCCGGGCGAATGAGTGGTCCAGTACCAGCATGTGTTACACAGAAAT
CTCATTTATTTGGCTACCATCGCAGATGCCAACCCC

SEQ ID. NO.: 47

pKVC92:

AGACCAGCCGGTGACAACCACTAATCAAGTTCCATAACTATATAGCGCCGCAATTCCCATGGCCTCCTC
ACTAAAGAACCCGTGAGTCACCTGTATCATAAATCACCCAATCACCTGCACCGTTAAACTTAAATACGAC
TTCTACCTCATCTTCCTTTAAATATAACAAGCAGTTAATAATTCTGCTAACACCCCCGTAATAAACAT
TGCTAGTA

SEQ ID. NO.: 48

pKVC8: TGAGGTTGATTATTGTGGTGGTATTGTTCACTGTGTAGAAATAGTAGGAGTA

GATTTAAATAGATTGTTTCAGTTTTTAAATATTAGCCATAGAACTGGTTAGTATCTCAGTAGTTTCATGAA
AGCTTTTCCTGTATTCTAATCTATTTTGAGAAATTTTCGTCCCTTTTTTTAATTGTGTCTTACAGTTC
AAGTTTGTAGATTTTAAATAAGCAACAATTTTTAAAGATGCGGTAATCTTCCAATAATTTTATCCATC
TTTCATGGCCCCACAACCTGCATCTTTAAT

SEQ ID. NO.: 49

pKVC8B:

CTAACTGCATTCTCTCCTCGTTCATCCTTTGGGGCTGATTGATGAGCCCCTTATTTCTTATCTCTAAAA
ATCAACAGCAAGGTCTACTTCACATGGCCACTCCAGTCCTTTGAGCTATAATCAGGATTATATAACTTA
CCCTCAAATCAAAAGTTAAGAAAAAGGAAGCCCATAAGCTAAGGCACTGAATCTTTTCCTGACAATTC
TAGAGGTAGAATTTTCATCATGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAAGGAGGGGAGGGAAG
AGAAATGAAAGAG

SEQ ID. NO.: 50

pKVC14:

ATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCCTTTCTTATTTTAAATAG
TACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATCCATGCAATCATTCAAGATTAGTTGT
GGTTAATTCTACTATGGCCACTTCTCGCTTGGATGCGAAAGCTTCTCACACTATGAAAACCTATTAACAT
GACTGCTGTTAATGAGATGAAAGAGCCCATTGAGGAAATCGTATTTCAAGTTGTATATGCATCTGGATA
GTCAGAATAAC

FIGURE 5G

SEQ ID. NO.: 51

pKVC16:

TGGTGACACACGTCTTTCAGTCACCAAGTGGAGATCACCAGGAGCATCAGCAGGAAGAGCCAGTGGGCCC
ACAAGCTTAGCAAGTTGATCAGGATAGGGTTATTTGGTGGATAGACCATGAGTGTGAGGGACCTCCAC
TGGACACCACCCAGAGGCTCAGGATGCTTTTCGAGGGAGGAAAGGAGAAAGACCTCTACTGAGGGAAC
AGCTGGCCGTGTGTGGTGGGCTGAGGTGACGTACAGGGGCAGAGCTTTCGAGGGATTTTCAGATGATCC

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FIGURE 5H

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SEQ ID. NO.: 52

pKVC20rB:

TAAATAGAAACGTATAGAATAGTCAAACCTACGTCTACGAAGTGTCATATCAGGCGGCGGCTTCAAATC
CGAAGTGGTGATTTGATGTAAAGTGATATTTTAGTTGGCGTAAGAAGCATACAATTAGGAAAGTAGAGC
CAATAATTACATGTAGCCCATGGAATCCTGTGGCCATGAAGAAGGTAGATCCGTATACTCCGTCCGAGA
TCGTGAATGATGTTTCATAGTATTCTGGAGGCTTGAAGGAGTGTAAGTAGACTCCTAAAGAGATTGTA
ATAAATAGTGCTTGAAG

SEQ. ID. NO.: 53

>pKVC59BR

poly(T)GTTTTTGTTTTTAAAAATGAGTTCTTTTAAAACCATGTCATACATTCCCCATACTGATATCG
CATGACCCNTTANAATAAAGGCAGGGGGNTTACTAATGGGGGGGCGGGCCANACCCNCCATCGTTTCA
GCCAGACAGTTCAACCCGGGGNNCCTTGTTCTGCGGACCTCCGGGGNANGCCTTTCCTTTTCCAAAAA
GGGGGCCGNTCGGAGNATGNATNTNGAGGGCCCAATTAG

SEQ ID. NO.: 54

pKVC21B:

GCGCTCTGACCAGGCATCAGTTTTCTGGTGCTCTCTGGGCTAGCCTGGTGATGTAGGGCCAGGCAGAC
AGGCAGGCAGGGGCTGAACAGGGTTTCTCTGCTCCAGGAAGACCAAACACAGAGGACCTTACAGGCAGG
AACCCACAGACTGTCCCAACCCACACACTCCACCACCTGTGCCCTGTCCCATGTCTGAGCCAAGGCC
TGAGGTAGAAAGTCACCTGATCCTGTATCTCCATAGGGGCCTGACTTT

SEQ. ID. NO.: 55

>pKVC61BF

poly(T)CCCNAGNGCACACNGGNGGCCNTAANNAGNGGNTCCNAGCNCGGNACCNAGNTTGAGGCATA
GCTTNAGNATTCNATAGTGNANCACAAATAGCNTGGGGNAATCANGGNCAAAGCCNTTCCCGTGNGAA
ATTGTNATCCNNTCANAATTCNCACAAANATACGGGCCNGAAGCATAAAGNGTAAAGCCCGGGGGGCC
AANGNGGGNGCNAACTCACATTTAATNGCG

SEQ ID. NO.: 56

pKVC23:

GGGAAATGTAGTTTGGATGCAAAGCTGATTAAATTGGATCAAGAAAAATTGGAATTAAATACATACAAT
AATGCATGCATTTATGGTTTCGATTTTATATATCCTTAGCTAGTTGGAAATGATGATTCCCACAACAA
GCATAACTCAGCTTGTTTCTGCTTACTGAGTACTTTCTCCTATGGTATATGTTGATAACATTTCTTCCA
TTATGTATGTTGCATAcgAGAGTTACAGTTACT GTGGAATCATAATTTT

SEQ. ID. NO.: 57

>pKVC9R

GTCACCATTAATGTCTgAATTTTaAACAGATTCTTGGACTGGTGGCTCATATCCATCAGCTCGCTCAA
CTTTAGCACCGGTCTCATCCCCAGTAGCTTTTCCAGAACTGCTACCTTCACCATGAAGCTCCATGAGCT
TTCCCAATTCAAACCTTGGGCTTCTCAGCATTTTACTTTTCTAACGAAGTCATCATGAAGTGGATAAA
TAGACTGACAAGCCTTCTCTATGTCTTTCCGATCTGTCTGGAATCAATTTATTGACAACCTTCTTTCAA
GTCA

FIGURE 51

09301507 1042899 668240 40570560

SEQ ID. NO.: 58

pKVC28B:

TCATAGCATTCTTCTGCTTCTCCTGGATTATGTGCTACAAATGTGCTTTGGCTTTAGAAAGGGATGGA
TGAGAAGACAGAGCTGAGATCAACCTGGGTAGAAGCAGAAAGTTAAACCCTTTAAAAGTGCTGAACACA
GATTCGAATCCAAATGGTTCAAGCAGCCATGAAATCGCTCTTCATGAAGTGGGCTTAATTCTCTAGTTT
AAGTTCTTTTGATGGAATGAATTAATTAATGTGTCAGGTGGCTTATTTGTGGATGCATGATTGATGATG
TCATT

SEQ ID. NO.: 59

pKVC29:

CGGACCCGGACAGAAAGCAAATCCTGGAGCGCACCCAGCGTGCGGTGGGGCTGGCCGCAGAGCCCCTGG
AGAGAGCCGTGCGGgNCGGCCTCCCGGCAGAGGAGGCCGCCCGCTGCGCAGAGGTGTTGTTGGAAGAAG
CGAAAGATTTGCTCTCCGACTGGTTGGACTCCACCCTGGGCAGCGAAGTTACGGACAATTCTATTTTCT
CCAAACTGCCCAAGTTCTGGGAAGAAGAATTCCACAGAGACATGGAAACCCTGAACGTTCTCCCTCCGG
ACGTCCT

SEQ ID. NO.: 60

pKVC38:

CGAATCTGTTGTAGCAGTTTCAAATGATTGTGTGGATATTGGATGTTTAACCTTTACCATTTGCTTTGT
ATCGACACATTTTTTCATTTTAAAGTGTTAACTCATGTACTGTTTACTTTAGGAATAATGCAAATCCAACC
TTCATCCAGTGATGAGAATAGCAGTATGATAGGAATTTGCTCAATGTGCTTTAAATGAGTAATTGCTTT
ATCTTTTTTAGTATCTGATAGACTTTGCATGACACGGTACACTCCTAATTATGCATTCTTTAGTTTCCA
AATCTTAACCTAAGACATTCTATATTAATGATGGGTAGCTGAG

SEQ ID. NO.: 61

pKVC48B:

GGTTTTGCAGGGGCAAGTGGGGCTGGGCCCCGCTGGGTGAGAACCCCGCCGCACACTGCAGTGGGTGCC
TGGACCCCGCAGCAGCGCTGAGCAGACGGTGGACTCTGGGCTGTGGCCTTTCTTGGGCCCCACTGGGGCC
GGCTCTTGATATAGCTGGGGCTCATGGGCATGACCCCTTTTTTAAACCTTGGGTCTTAGGACACCTG
GGTTTACCCTCAACTAAGGGAGGGTGGGAAGGGATTACTTGGGGTCTCAATAATTTACGATATCCCT
TTAAGGTTGACCATTAAACTGTCCCA

SEQ ID. NO.: 62

pKVC51B:

CCTCTTAATAACCTCAGGCCTGGCTATATGATTCCACTACAACCTCAACACTGCTGTTAACCCTTGGAAT
AACTACCAACCTACTAATATATATCAATGATGACGAGACATTATCCGAGAAAGCACATTCCAAGGCCA
TCATACACCTATCGTTCAAAAAGGCCTTCGATACGGAATAATCCTCTTTATCATCTCAGAGGTATTCTT
TTTCGCAGGCTTTCTTCTGGGCCTTTGTTACCACTCAAGCCTAGCCCCAACCCCCGTAGCTTAGGGGG

SEQ ID. NO.: 63

pKVC53B:

FIGURE 5J

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SEQ ID. NO.: 69

pKVC69:

TGGCTGTCTCATCTGGAGGCTTCTGCCTCAGCTCCTGAAGGCTGCTCTCATTCTTCTCGCGTGCTCCCGT
CCATCTTCAAATTCTCAATGGCCCATCTTCTCACGCCTCCCATCCCTCTGCCTTCTTCTCTGTTTTAA
GGTTCATGTGATTAGATCAAGCCCACTGATCAAGTCTCCCTATTTTAAGGTCAGTTCTGCCATAGAACA
TAACATAATCACAGGAGTGACTGCACAGGCACGGGTTCTGGGATTGGGCATGGAGTTGGGGG

SEQ ID. NO.: 70

pKVC74:

ACGCTAAGGACACCTTTTTTGTCTGACCTGATGTTATAGATGGCAACACCAAGTTCTAGAGCAATT
GAGAGACTTGTCCAAGGTCACAGGATGGCTTCACCTCAGCCAACTATATAGTTGCAGTGACAGTATGTG
TGCTCTCTGAGGGGTTACTGAAAACCCCTGTCAAATATTTCTGTGGACACTCAGCCTTTAAACTCCCA
AGCCTCATGAAGAACTTATTGGGGGGGGGGGGCGCCTAAATAATTCAGTCGGTTGAGCGTCTGACTTCG
GCTCAGGTCATGATCTCACAGCTC GTGAGTTCGAG

SEQ ID. NO.: 71

pKVC86:

TGCCTAGAATCATTGTTCTGTGTGGAGGTGTTTTGTTTTGATAGAAACCGGCCAGTCTTGAACCAGAAC
GAATGTTTCCCTTGTCTAATGTTCTCACAGAGAAATGGACAAGCGTTTTACAGGTATAAAAGGCACAAG
GAGGAACCTATTTTTGGTCAGAGCATTGGGGAAGTAAATCACAAGGCAAAATAGATCTGTTTGTGTTT
GTTGCGGGAGGAAGTATTAATAAGCAAATCAAATGCCTTGTATGATCTCCAGTGTTATAATTATAGATC
CTAACTTTGCAAATACATGTAG

SEQ ID. NO.: 72

pKVC96B:

ACTGGACCAAAATTGGTGTTTGTTTTAACTTGACTCTTCTTTTGATTATTTCTAATGCTACAAGAATG
CTGTAAAGTGCTTCTACAATGATGTAGCCCTGACAAGACATGTTTGGCAGTGTATAAAATTAGGTAG
GATTGTGCACTGATTGACCATTTGTGAAATCTTTTCTCAGTGGAAGTGCATTCTCTAATAAAATTTAT
GNAGGTGAAACAATCTTTGGNGCAATGGACCACTCATGCATCCATCCC

SEQ ID. NO.: 73

pKVC97B:

AACAGCCCCACTATCAGCACCCAAAGCTGAAATTCTTTCTTAACTATTCCTTGCCAATACCAGNAAAG
CAACCCATAACTTTTATAATTATATATTGCATATACCCATACTGTGGCTTGGCCAGTATGTCCTTAT
TTCCACAAAAAACCAAGTAANAAACCCCAAGTACCACAACCCAAAACACACAATGTAAATCACTCT
ATTAACCACANACCCACCCAGGTTGGGTATTATACCCCATGGTNCATAAGGACATACTATGT

SEQ ID. NO.: 74

pKVC103rB:

CGCTGCATCTTTTTCTATGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTC
GTNTCATGATCGACTCGGACCCCTCTGCGNCTGCATGAGGGACCACTATGTTGNATTCTATCAGCTCACC
CGTTGNTACAAGTGAGNCTCAAAGGAAGAATAGTGGGAGTCTTCTGTGAGACCTATCTGAATCCCCGN
NTGGCCCTGAGNTTCCAGAGGGNCCTGGTTCGTCCTCGCTAGCAGGGTTCAAGNAAAGGGGCCCGCN
CATGGCAGTCCTTGGNCAGNAGNAANGGANTTGGNCCCAACCCCNNTGGTTCCCAACCCA

SEQ ID. NO.: 75

FIGURE 5K

09301507 042339
663240 70510660

pKVC103:
CGGCCACTGGTCATCAGATGAGCATTTTGTGTGTTTGAAGCTAGTAGCTATAGAAAAGATAGTTGTGCC
CTGATAAAGTAGCTTTTTTAAAAAAGTTTGGGTAGTTTACATTCAAGGGGCTTATGAAGAGATGCAA
GTCAGGATACATAGGCTTGATTCTTGGCAGCTTAATGAGTCTTCACGAGGCACTGAAGGTGGAAGGGTG
GAGTCCAGTAACTGCTCTGGAGCAGTGACTTCCCAATTCTGACGATCTCAACATTGTTTCTGAAGGACG
TTGCCATCTTGGACACAGGAACGTGCTGTGGGGTGCCTGGCAGTGTCTGAGTAGTAGACTT

SEQ ID. NO.: 76
pKVC104rB:
CGCTGCATCTTTTTCTATGCTCTCCCTGCTGGCGCTGATGGGAGATACAGACAGCAAAACGGACAGCTC
GTTTCATGATCGACTCGGGACCTCTGTGCTCTGCATGNAGGGCACCACCTACTGTTGGATTCTTATCA
GNNCAACCCGCCNGNTGCAAAGATGNTAGACTCCANAAGAGNAAGNAATNAGTTGGGGNAGGTCNTTT
CCTGCTGNAGAACCTAATTCTTGAATTCCCC CCCC GCCCCCCG

SEQ ID. NO.: 77
pKVC107fB:
ATTACAACATCTAGAAGGCTTTCATCATACGATACAAAGCTCAGTTACAAATGTGCATCCTAGTATTTG
GAAACTAATACCTCTCTTAATGTAAATGAAAAAATTATTTCTTATGTCCTTTTTTCAGGACTCCTCTT
TTATTTTTTGGTATTTTATCTTTTATGGCCACCTTGGCCTTCTGGCCAATGTGTTATGCAGTGAAAATG
CTTGTGGGCAGAGGATGCCCTACAGCGCAAAAATACCGCGCACATGGGTTTCCCAGGTA

SEQ ID. NO.: 78
pKVC107rB:
TTTTGTTTTATCCGTTTATTAGTACATGGGCGTCGGGAGGATGATTTACTCATCATCTTGTATTACCAG
AGGTAGAGCATAATGCCATCTGCTAGGGATCCAGTTCGACAGCACCTCAAAACACTAGTCTGCTCACTC
ACCCTATAGGGCTTGNTCATTCCACTTGGGATGGAAGACAACAGTGCCTTTAATGCAAATGGGCCCCAG
GCAAGGAATTAACCATTTGGCTTCATGGCTCATGAAGGAATACAGNCNNATTTAANGCGNGGCAGGCAGG
AAGCCTTTGNGCTA

SEQ ID. NO.: 79
pKVC124:
CTAAAGTGGCTgAACAGTATACCCACCCCTAGCCGGCAACCTGGCTCATGCAGGAGCATCCGTAGACCT
AACTATTTTTTCACTACACCTGGCAGGTGTCCTCCTCAATCTTGGGTGCTATTAATTTCACTACTACTA
TTATTAATATAAAACCTCCTGCCATGTCCAATATCAAACACCTCTATTTGTCTGATCAGTCTTAATCA
CTGCTGTCTTACTACTTCTATCACTTCCAGTCTTAGCAGCGGAATCACTATATTATTAACAGATCGAA
ACCT

SEQ ID. NO.: 80
pKVC24B:
GCCGGGAGCCGGCCTTTGGGCCGNGGGCGGAGAGGCCCGGACGGTCGAGTGCTTCTCCTGACTGGTG
CGAGAAGAACATTTTCTATATACTTCCAGGTGCTTTTATATTCCTTTCGAGAAGAAAATAAAATTATGA
ACTCAGGATTTTGCAAGTATTCTGTGTTTCTCCTGGAGTAGGTAGTCCTTCTTCTTTTACCCAGCCACT
TTCCCTATTCTTGAAATGTGGATCTCTCTTCTCTACATGTTTTACCTCCATGATTTGGATTGGAAAAAG
CTGCTTTTCTTTTGGTTCCACTTTTTCAGATTCAACATAGAGAAGCTCCTAGGATGCAGTCGTCTTTCTG
AAGCGCTTCCAGGGAAGAAAGAAAGAAACT

FIGURE 5L

668240 40570560

SEQ ID. NO.: 81

pKVC25:

AGGTCTTAANCCCAACCCCGTCCCACCCACAGGGTNCCAGCGTGGTGA
CTACAGGCGACCCTCCCTATGTCGGGTCTAGAACGCCCCCAGCTGGAACGAAGGGAAGAAGCTAATTACAGTGTCTTCCTTTGCACTGAC
CNNCCCCCCCCCGCCCCCGCCACCAGTTTCAGTCCAGGAGGGGACTTGTTAGCCCGTAGCCCATCTT
CCCCACTATCCTGGCGTGTGGGCTCGTGAATGCCTCCTAGCCAAATCACTAGAGTGCAGTGACCCAG
CCTCCTTCCTGTGCCAAGATG

SEQ ID. NO.: 82

pKVC40B:

GCAACAAGGAATGAGACCCCAATGCCGCCTCATGGTCAGTACGGTGGTCATCATCAAGGCATGCCAGG
TTACCTTCCTGGTGCTATGCCACCGTATGGGCAGGGACCGCAATGGTACCCCTTACCAAGGTGGGCC
TCCTCGACCTCCGATGGGAATGAGACCTCCTGTAATGTCGCAAGGTGGCCGTTACTGATCTTACTTCAT
CCAATCTAATAGGTTTTGAGATTAAACCTTTTCTCAACTTGTGCTGGTTTATATAGCCAAGCTTCCGTC
AATAAGGCTTTATTGTTGACTTTAACAAACATTATATTACCACATACCAGGGACTATTGGACAATTATT
TTACAAGGGGAAAATT

SEQ ID. NO.: 83

pKVC43fB:

CCTGGCTGCCTGTGCCTCAACCCCACTCCCAGGGAGACCAAAGCCTTCATACATCTAAAATTGGGGGG
GGGGGGGGGACAAAAAAGGGGGGCCACGATGGCAGACCATTGAAATAAAACAAAAAGACCAAGTTTT
AAGGCGAGAGTTTTAAAAAAATTTGGACTACATAATTTACACCAAGGCAATGTTATCACCTGCGCCTG
TTTGGACTTGGGCGGGGACTGGCCCTTCTCCTCAGGGGGAAATGGGGTGGCTTTTGGGAAGGCAAGGGA
CTTCCTGTAAACATGCATCTCAGGGTATTTGGAATGACTATTAATAAAAAAAGGGCCAATGTTACAGTC
AAGGTCCTGGGCCCA ACCTTGGAACTTTTGGGGGT

SEQ ID. NO.: 84

pKVC55B:

CCCAAACATCTACAAACACAACCTAACACCAGAAAAATAAAACAAAACATTTAGTCACCTTATAAAAGTAT
AGGAGATAGAAATTTAACTTGGCGCTATAGAGAAAGTACCGCAAGGGAAAGATGAAAGATAAAATTTAA
AGCACCACACAGCAAAGATTACCCCTTGACCTTTTGATAATGAGTTAGCTAGAACAACCTAACAAAG
AGAACTTCAGCTAGGCCCCCCGAAACCAGACGAGCTACCCATGTACAATCTATTTTCAGGGGTGAACTC
CGTCTATGTTGCAAATTAGTGAGAAGGTTTTTGGGTAGAGGTGAAAAGCCTATCGGGCCTGGTGGTAG
CTGGTTGCCCCGAACCGGATTCTTAGTTTCACCTTTTAACTTTTCCT

SEQ ID. NO.: 85

pKVC57B:

GCGGAAGCAGTGATCCTCCAGCCTGCAGAGGCCCTTCCCCAGCCTGGCCCAGCTCCGGCCCGGCCCC
GGGCTGGACTCCTCTACAGATTTATTTGACGTTTTATTTTGGTTTCCCCACACCCCTCAATCTGT
CGGGGAGCCCCTGCCCTTCATCTTGCTCCCTTGCCAGGAGTGAGTGACCCATGGCCTTGCGGAAATTG
TCCTCCTCTTCTCCCTCGCACTACAGTCTGGTCGGGGAGAGGGTGGCGGGTGCTGCTTGTGGTTTAG
TGGGTTTTGTTTGGTTTTTTGTTTTCTTTCT

FIGURE 5M

SEQ ID. NO.: 86

pKVC60fB:

AAAGGGTGGGGCANTTGATGCTGGTTTCTTCTCTGCGTTTTCCGTAATTCCTTCTTACTAGGGCTTTA
TAATTCTAATTTTTCTTGGTTAAGTAGTAATATAAAACACAATCAGGAACACTCTTTCTTTCCAAGTAG
GATGCAATTAGTCCAAAGTTTTTTGGATGCTGGATAAACTTGTCTTAAAGATCTCCTTCTCGTGGTCA
GTCCAAACATTCAAACTGCCTATCTTTATAAACTTTCATAGGATCTCCATGAGTCCATTTCATGTTG
ATGAATTTGACTCGTCTCTGTTCTGCATCAAACATCATAGGTGGGATCACAGAGAGTTGCCGCATTTGT
TTCTCATTATTTCTCCTTCTCAGAGAGCCCATCAATAATTTTCAG

SEQ ID. NO.: 87

pKVC60rB:

GTTTCCAGAAATTCGAAAACAAAGAGAACAACAAGAAAGGTTTCAGCGAGTTGGGCAGAGGGGAGCTGG
TCTTTCAGCCACGATTGCTAGGAGCGAGCATGAGATTTCTGAAATTATTGATGGGCTCTCTGAGCAGGA
GAATAATGAGAAACAAATGCGGCAACTCTCTGTGATCCCACCTATGATGTTTGATGCAGAACAGAGACG
AGTCAAATTCATCAACATGAATGGACTCATGGAAGATCCTATGGAAAGTTTATAAAAGATAGGCAGTTT
ATGAATGTTTGGGACTGACCACGAGAAGGAGATCTTTAAGGACAAGTTTATCCAGCATCCAAAAAACTT
TGGGCTAATTGCATCCTACTTGGGAAAGAAAGGGTGTTCCTGATTGTGTTTTATATTACTACTTAACCC
AGGAAAATGGGGATTATTAAGGCCTAGTAAGGAGGGATTTACGGGAAACCGCAGAGGAAGGAACCCGC
AGGCAATTGCCCCCCTTTGG

SEQ ID. NO.: 88

pKVC63B:

CCTACCCGGTTTTGGGATAATCTCACATATTGTTACCTACTATTTCAGGTAAAAAAGAACCCTTTGGCTA
CATGGGAATAGTTTGAGCCATGATATCAATCGGCTTCCTGGGCTTTATCGTATGAGCCCATCACATGTT
TACTGTAGGAATGGATGTAGACACACGAGCATACTTTACATCAGCCACTATAATTATTGCCATTCCTAC
CGGGGTGAAAGTATTTAGTTGACTGGCTACTCTTCATGGAGGTAATATTAAATGGTCCCCTGCTATATT
ATGAGCCTTAGGCTTTTATTTTCCCATTTACCGTAGGAGGGCCTAACGGGGATTGTACTAGCAAACCTCT
TCACTAGACAATGTTCTTCACGGCACATATTACGTGGGGGGCCACTGTCACTATGGCTTGTCAATAGGG
GCAGTATTCGTATCATAGGGGGGTTTCGTCC

SEQ ID. NO.: 89

pKVC64B:

GCAATCCTGGCCTGGGGGCCTGAGGCCCTTCCCCTGCTCCAGGCTGTCATCTCCTGCCTCCTCTCCTCC
GGCCTCCTCAGTTTGGCCAACTGCAATTCATTTGAGTTACTGTTTATGCTAAGCATGTACTCCTGACTT
GTCATGACTTTCCTCTGGAGCAGGTGGCTAGAAAAAGAGGCTATGGGTGGGGGAAAAAAATGTTCTGT
TTCTCACTTGTAAGGCTGGTTTTTGGCTTTTCTGCCATGGGATTCTCCCCCTGACCTCTCCCCTCAGCA
ATTCTGCAAAGGGTTAAAAATTTAACTGGTTTTTNACTACTGATGGACTTAAACAACACAAAGGATG
CTGGGATGCTAACTTGGTTAACTAAACCATCAAGGTTGTACCAAGTTTGGATTGGTAACTGGTNAAAT
ACAACTA

FIGURE 5N

SEQ ID. NO.: 90

pKVC66B:

CGTATGAGGCAGTCCCCTGCTCGCCCCATCCCCACTGTCAGGTCTATGGGTCCGTGGGCCAGAATGGG
GTGGAATTGGGTTGAGGGAGGGACAGCCCTGGCTGACAATGATATTGGTGTAAATCAACATTAACCGAGC
CGGCTTCAGCTTACCTCAACCCGGGCAGGACACCACCACCTTGAGAAACCACAAGCTGGAGCGACCCTC
AGGCCCTGCAGGCCTTGCAAACAGCCCTGGGTGGACCCACACCAGTCCCTGTTAGCCAGCTAGGCCCA
GTCTTCCTTCAGCACCACACTTTTATCCTGGGCAGGTTTCTGTGAGGTGGAAGCTGGTAAAAGCGGGTC
CCAGCCAAGGGCTTCAGGTTGAGCGCCAGCCAGTAACCTCAATTCTTAACGGTGGGCAGGA

SEQ ID. NO.: 91

pKVC82B:

GCCACCTGACCCTCCTAACCCATGGCTGTCTGATGATACTACTTTCTGGGAACCTGNAAGCAAGCAAAG
AACCAAGTCAGCAGAGGGTAAAACGATGGGGTTTTGGCATGGATGAAGCATTGAAAGACCCAGTTGGGA
GAGAACAGTTTCTTAAATTTCTAGAGTCAGAATTCAGCTCAGAAAATTTAAGATTCTGGCTAGNCAGTG
GAAGNACCTGAAAGNAAAAGGTCTAATNAGGAGAAAGTTCCCTTTCCCGGAGATTGAGGGAAAATATGG
GCAAAGNAATTTTCTTGGGCTCCCTGGGAGGCTTCCCAGNTGCCCAATCCAAACCTTGGGGTTTTCT
NAAGGAGGCTNATGGATT

SEQ ID. NO.: 92

pKVC110

GAGAAAGACATAATGGTTATGGCATTGGCTTGAAACCAGTTAAAGAGGGTTCGATTCCTTCCTTTCTTA
TTTTAATAGTACGTAAGTTGGCTCTTCAAATGTGTGGTACGGAGGAGGACATC_cATGCAATCATTCAAG
ATTAGTTGTGGTTAATTCTACTATGGCCACTTCTCGCTTGA TGGCAAAGCTTCT

SEQ ID. NO.: 93

pKVC134: Homologous to human alpha tubulin; Accession HSHA44G

CCGCCAGTGTGCTCTAAAGTGTGGTACCCTGGTGGAGACCTGGCCAAAGTACAG
CGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGGCCTGGGCTCGC
CTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTGTTC_cACTGGTATGTGGGTGAGGGCATG
GAGGAAGGAGAGTTTTCTGAGGCCCGTGAGACATGGCTGCCCGTGAGACATGGCTGCCCTTGAGAAGGA
TTATAGGAGGTTGGTGTGGA

SEQ ID. NO.: 94

pKVC108: Homologous to Mouse Initiation factor eIF-4A;

Accession MMEIF4AL

TCTTCTCCCAAAAACACTAATCCATGTCCGTAACCCACTCAGCCTCCAGACCCAGAGGCTCTCCCCCA
CCCAGCTGCCACCTCTAAAGAGGATTCAAGGGGCTATAGTGT_cACCCAACCTCATTTGCTGGACCAAA
TCTGGAGAACC_cTTGAGCTAGGTGGCC_cATGGGgTTGTCC_ccAGGTGGGgAGCAGGGGAGAGAAAATG
GTAGCCATTTTACATTGTTTTGTATAGTATTT ATTGATTCAGG

FIGURE 50

SEQ ID. NO.: 95

pKVC105B: Homologous to Human mRNA for proliferating cell nuclear antigen; Accession HSPAG

GTCAGACACAACCTTTCTGAATCCTCTNAGGANGGTGATCCAGTTCATGAANATTCTCTGTAAAATNANT
NTGGNAACTANATNAGTGNNGATNCAGGTCTNGAGNNTCTCCTTCCAGTGNCTAAAAAGTNCACAGAN
GNCAGGAACTNCCTATCTGCATGCAGTCACCAGTTCTCATNC TCTANGCA

SEQ ID. NO.: 96

pKVC92B: Human Mitochondrial hinge protein; Accession HSHINGE

CCCAGCCTTCATGAGCTGGTCATCAGGATACTTTCTTATGGGNTNGANCATGCCANTTGCTTNTNCGNG
TANATGTAAGTTCATGNCAACCNCATTTTTTTCTAGCCTNNGGCTNAAGGTNANTCGTCTCNTTANG
CAGCNGANNAGTTGNAGTCTNTCAAANGNNCACAAANACCTAA

SEQ ID. NO.: 97

pKVC91: Homologous to Bovine NADH dehydrogenase; Accession MIBTXX

GGGTAAAGTGATAGGAGGAGAAGGGCTGAGTAGGTGGAGGCTATTAGGGCATTCTCGGTGTAAATG
ATGGGTGATATTTTAAATGTGGTGTGTGATTTGCCTCGTTGAGTTATAATAAGTATGTAGAGGgaGT
ATaGccCTGTAATGATGATATTAGTACCCATTAGGATAATGGTTATGTTTGATCATGAGAAGGAGGCTA
TTACTAC

SEQ ID. NO.: 98

pKVC90: Homologous to Human hnRNP core protein A1; Accession HSRNPA1

ACAACCTTTGGCCGTGGAGGAACTTCAGTGGGCGAGGTGGCTTTGGCGGCAGTCGAGGTGGTGGTGGAT
ATGGTGGCAGTGGGGATGGCTATAACGGATTTGGTAACGATGGAAGCAACTTTGGAGGTGGTGGGAAGCT
ATAATGATTTTGGCAATTACAACAATCAATCTTCAAATTTTGGACCCATGAAAGGAGGAAATTTTGGAG
GCAGAAGCTCTGGCCCCTATGGTGGTGGAGGCCAATACTTT

SEQ ID. NO.: 99

pKVC86B: Homologous to Rat Ribosomal protein S27; Accession RRS27

GCGAAGGACCTCCTGCACACGTCCCCGGAAGAGGAGAAGAGGAAGCACAAGAAGAAGCGCCTGGTGCAG
AGCCCCAACTCCTACTTCATGGACGTGAAGTGGCCGGGTGCTACAAAATCACCACCGTGTTTCCCT

SEQ ID. NO.: 100

pKVC82: Human Carboxypeptidase E; Accession HSCARBE

ATCTGCCATTTTAGACTTAAAGGAAATATTCCACGTGTTATTTACGATCCAGAAGTTTTTGAGTAATTC
TGGCTTTTAAAACTAATGAAGTCCTTTTAGTGTAATGGTAACAGTGCCACATAGTGAATGCCACTGAA
AAGGTCAACAGCTACATTTTGGTGTTGTGAGCATTATACCGCAAGACTTACATAGTTTCAAGTATAA

FIGURE 5P

SEQ ID. NO.: 101

pKVC80: Homologous to Rat VAMP-2; Accession RNVAMPB

GGTCCTTGATCACTTTTCATTTGCATGACGTTCTTGACAGGTGGTGGGAGCCTGGGCTTTTGGGGAGCC
AGAACCTTCTGGCCCCCAGAATCACCCCTCCTAGCCCCCTCTAGTCCAGTTTGCCTCCCCTGCCCCCA
TTTTCCAAACCTCTTGTCCTCTCCCTCCCTCCCCCTCCCCCAGCTGGTGTGGAAGTGTCTCGGAG
TTCAGTGTGTATGAAGGACAATAGTTTGCACCTGGAGTTT

SEQ ID. NO.: 102

pKVC79: Homologous to Bovine Nuclear encoded ADP/ATP transporter;

Accession BTADTPMT

GGATGATTGCCAGAGCGTGACAGCGGTGCGAGGGCTGGTGTCTACCCCTTTGACACTGTCCGCCGTA
GATGATGATGCAGTCTGGCCGGAAGGGGCGGATATTATGTACACTGGGACGGTGGACTGCTGGAGGAA
GATTGCAAAGATGAGGGAGCCAAGGCTTTCTTCAAAGGTGCCTGGTCCAATGTGTTGAGAGGCATGGG
CGGAGCTTTCGTATTGG

SEQ ID. NO.: 103

pKVC59B: Homologous to Rat scg10; Accession SCG1_RAT

ACGACTCACTATCAGGGCGAATTGGGCCCTCTAGATGCATGCTCGAGCGGCCGCCAGTGTGGGAAAAGG
AGAGGCATGCCGCGGAGGTGCGCAGGAACAAGGAACTCCAGGTTGAACTGTCTGGCTGAAACGATGGAG
GGTATGGCACGCCCCACCATTAGTAAATCCCCCTGCCTATATTATAATGGTTCATGCGATATCAGTATG
GAAATGTATGACATGGTTTAAAAAGAACTCATTATAAAAAACAAAAACAAAAAACAGAATC

SEQ ID. NO.: 104

pKVC55: Homologous to Human LAMP-1; Accession HSLAMP1A

AGCATGCTGATCCCCATTGCCGTGGGcGgCCTGCGGGGGCTGGTCCTCATCGTCCTCATTGCCTACCTC
ATCGGCAGGAAGAGGAGCCACGCGGTACCAGACGATCTAGCAGGGCTGCGACACGTGGGGCCGGCTGC
CACTTCCGGTCTCCGCTCGTCCCCTGAGCTTAGGTTGGCGTGGAGGGCGGCACGTTTCTTGCAAACCTG
ATTTTCAAATCTGCTTTATCCGATGTGAAGTTCATCTTGCAACATTTACTATGCACAAGAGTATTGAAA
TGAC

SEQ ID. NO.: 105

pKVC49B: Homologous to Chicken Contactin; Accession GGCONTAC

TTCATTATGAAAATATCAATAAATATGTCATTAGTTTACATTCAACTCTTTGTTATAAAATTAACTTT
TTAATAATAAGTGAAATGGGTGATTTCCCCCTGGAGGGATGTCAACAGGCTTAAATCATTTCCTGGTT
TCATAAAATACAACTCCTTTGAAAAAGGGACAAAATCTCTTCATACTTTTGGGGAACGGATACTGTGT
AAGCCCTCTGTACAAAAGTTTGGGGTTTTTATTGTTACACTTTGGGGGTTTCCCTTTTCAAGGGGCCCC
CCTGTGGGGGGTTTTTTTTTATGCGGGCAACCAACTAAATTTTTTTTCCCAAATGGAATGCCCCGCCC
TTTTTTTTTCTAATGTTTTTTTGAATAAGGGGGGCCAAAACCGGGGGAGGGTTTTTTCATGAAAAGGGT
TCCTTAAGGGTGAGGGGGAACACGCTTTGGGGGGGGTTTTTCTTTTAAGTTTGTGGCCCCAGTAGGG
GGGAGAAAGCCCTCCCCCGGGAAACCAGGGTTTGGTTCCCCACGG

FIGURE 5Q

SEQ ID. NO.: 106

pKVC47B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCCATG
GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC
AAGGGAAGTAAATACAACATTGCACTTTATAAGCACTGTATTGTTAAGTGGGAAATGCAATGTCTTTAA
AATAAACTGTATTTAAAATTGGCGCCCCAAAA AAAAA

SEQ ID. NO.: 107

pKVC46B: Homologous to Human 71 kD heat shock cognate protein;

Accession HSHSC70

CCTGAGAATAGGTCTAGCATTGTTCCACACAAAACATTTGAAGGACCCAAATTTGTAGCAAATTCCATG
GCAGTGAAGTTGAGCTGCTATAGTTAATAAACTGGGCATTCTTGATACTTGAATATGGAATATGTGCAC
AAGGAAAGTAAATACAACATTGCACTTTATAAGCACTGGTATTGTTAAGTGGGGAATGCAATGTGCTTA
AATAAACTGTATTTAAAATTGGCACCAA

SEQ ID. NO.: 108

pKVC35B: Homologous to Human Vacuolar proton ATPase channel;

Accession HSPCHSUA

CTTTAGAGGACACACACNCACGGGGCCGCCGCCCCCAGTAGTCGGTCTTGTAATGCGCAGTGTCTTA
GTGCCCCGTTGTCTGCTACCCCGGCCTCGCCCCCGCCCCGCCCCGTGCCGTGGACATCCGGGGCCCACTCC
TTACCCATCCGGGCCTCCGGCCCCCACTCATCTGCCCTAGAGCGCTCTGTAGAAGGGTGAATTAGAGTT
GTATTTCTCTTCACTGGATGTTTCTTATTATA AAGATTGATCTGTTC

SEQ ID. NO.: 109

pKVC27B: Homologous to Rat Cytoplasmic Succinyl CoA synthetase;

Accession RNGLTA

GCGACACGTTCTGTCATTTATGTTCTCCTCCTTTTGCTGCTGCTGCCATCAATGAAGCTGTTGAGGCG
GAAATGCCCTTGTTGTGTGCATTACTGAAGGTATCCACAGCAGGACATGGTGCGGGTCAAGCACAAA
CTGCTGCGTCAGGGAAAGACCAGGCTGATCGGGCCTAACTGCCCTGGAGTGATCAATCCTGGAGAATGC
AAAATTGGCATCATGCTGGCCATATTCACAAGAAAGGAAGAGTTGGTATTGTGTCCAGATCTGGG

SEQ ID. NO.: 110

pKVC22: Homologous to Human clq beta isoform; Accession HSC1QBR

GGAAAGATGGGATTGTATGAAACACTGCATTTACAGCAAAGACCTCAGTCCAGAACACAACACAGGGG
ACCAAGTGGATTGAGGTGTGGTCAAACTCTGGGGATCACAGTGGGGATACCCTCCAGGGCTGGTGA
CAGATTGAGGACCCTCCTGGCACACCCGGGACCCAGGGATAAAAGGAGAGAAAGGGCTGCCAGGGCTG
GCTGGAGACCATGGCGAGTTTGGGGAGAAGGGA GACCAGGGATTCTGGAATCAGAAA

SEQ ID. NO.: 111

pKVC22B: Homologous to Human Phospholipase A2; Accession HUMPHPLA2

TTCCAGACGGGAGATTGATTGGAAAAAAGTAATGTGTTCCATTTAAAATTTTGGTATATGGCATTTT
CTGACTTAGGAAGCCACAATGTTTTTGTCTTGGCCCATCATGACATTGGGTAGCATTAAGTTTTGTGC
TTCCAAATCACTTTTGTGTTTAAAGGATTTCTTGATCTTGTTATAGCCTGCCTTCAATTTTGATCTTTAT
TCTTTCTATTTGTCAGGTGTACAGGATTACCTT TTTAGCCTTCTGTCTT

FIGURE 5R

463470860

ACCCTTTCTATGTGTTTTATCTAATTATTTTGGTTGTTAATATGGTAATAATTAAGTCAAGGTAAA
TTTTAAATATTAAGATTTCTGATTTATTGAGCTTGACTTATGCCACCACGCTTATGTAAAATGAAAGTA
GCACCATGGTGAAACTGAAAAAGTTGCTCAGTTGTAACAGTTTTGATTTATTCTTTCTTGACCTCT
TTCCCTTATTGTCTTGAACCATAGCAAAGGATACTGCATCTCTTAATAATTGTAGTGCTGAGGTATT
GAaGTTATAT

pKVC18: Homologous to Human Cytochrome oxidase I; Accession MIHSCG
GTTATATTGACTCCTACAAACATAATCGTAAAGTGAATCTTTGCTCAAGTGTTGTCAAGGGTATATCCT
GAGAATAGGGGGAATCAATGGACGAAGCCTCCTATGATAGCGAATACTGCTCCTATTGACAAGACATAG
TGAAAGTGGGCCACTACGTAATATGTGTCGTGAAGAACAATG TCTAGTGAAGAGTTTGCTAGTACA

pKVC17B: Homologous to Rat SubstanceP receptor; Accession RNSPR05
GCTATAGACACAACACTTTCACT
CACCA

pKVC12B: Homologous to Human 90 kD heat shock protein;
Accession HSHSP90R
ACGCTCGTTTTCCAAAGAGAAGAGCGTTGTTTAGAGTAGCGAAATTCGAAGGCTGCTTAGGCGCATTGT
AAAGCTGTTGGGGAAATAACTCCACAAGTTTCGTGAGTGGAAATGTAGTGCTCGAAACACATTCTGCTT
TAAAGGTTGTAACAAATACAAACAAATTTAAAAAAGCTCTGACAAATGTTTTGTGTGGGAAGCGGG
GTTCCAAAATACAGGGCGGCCCC

pKVC10B: Homologous to Human Cytoskeletal gamma actin;
Accession HSACTCGR
TTGTCATCTCTTCAAGAATTGACAACAGATTTTGGTTTTCTACTGTCATGTGGAACATT
AGGCCCCAGCTTCGGCTCCTTGTGCGAGGAAAATAAA

FIGURE 5S

SEQ ID. NO.: 117

pKVC9: Homologous to Human v-fos transformation effector; Accession HSFTE1A

GCATCTGATGGCCTTAAGGGTCGTGTGTTTGAAGTAAGCCTGGCTGATTTGCAGAATGATGAAGTTGCA
TTTAGGAAATTCAAGCTAATTACTGAAGATGTTCAAGGCAAAAAGTGCCTGACTAATCTCCATGGCATG
GATCTTACCCGGGACAAAATGTGCTCCATGGTCAAAAATGGCAGACCATGATTGAAGCTCACGTTGAT
GTCAAACTACCGATGGGTATTTGCTTCGTCTCTTTTGTGTCGGTTTTACTAAAAACGCAACAATCAG
A

SEQ ID. NO.: 118

pKVC6B: Homologous to Chicken Amphiphysin; Accession GDAMPHIP

CCTTCCAGAACCCTGAGGAGCAGGATGAAGGCTGGCTCATGGGCGTGAAGGAGAGTGACTGGAACCAGC
ACCTAGAGCTGGAGAAATGTCGGGGCGTCTTCCCCGAGAACTTCACCGAGCGGGTTCAGTGAGGGCAGC
AGCTGCTGAG

SEQ ID. NO.: 119

pKVC6: Homologous to Human TAPA-1; Accession HSTAPA1

TCTACGACCAGGCTTTGCAGCAGGCCGTGGTAGACGACGACGCCAACAATGCCAAGGCCGTGGTGAAGA
CCTTCCATGAGACGCTCAACTGCTGTGGCTCCAGCACGCTCTCCGCGCTGACCACCTCCATTCTCAAGA
ACAACCTGTGTCCTTCAGGCAGCACTGTCATCAGCAACTTCTTCAAGGAGGACTGCCACCAGAAGATCG
ATGACCTCTTCTCGGGAAAGCTGTATCTCATTG GCAT

SEQ ID. NO.: 120

pKVC4B: Homologous to Rat alpha internexin; Accession#RNINTLAA

CACCTAAAGAGTTGCCAGGTCTCTGTACACATCTCCATTCACAACAGATAGGGTGTGATGCTTTTACT
AACTTTCTTATCCTAGGACCTGCTGCAATGGTTCAAGGAACTGGAAAGATGCTTTCTTCTTCTTCTT
CCCTCACTCCATCCCTGTCTTTACTCCTCAGACTTCCTGTAAACATTAGTAAGATAAGAATTAAGT
CACACGAATCCAC

SEQ. ID. NO.: 121

>pKVC154

ATTTGGCTCAGTGGCAGAGCGCTTGCTAGGAAGAGCAAGGCCCTGGGTTCGGTCCCAGCTCCGpoly
(A)

SEQ. ID. NO.: 122

>pKVC159

GGGAGGAGGAGGAAGAGGAGGAAGGAGAGGAGGAGGAGGAGGCTGCAAAGGCTCTGGGCTCCTCTpoly
(A)

SEQ. ID. NO.: 123

>pKVC151

GTAATTATTGGCTCAACTTTCTAATTGTCTGTCTACTACGACAACTAAAATTCCACTTCACATCAAAA
CATATTTCCGATTTGAAGCCGAGCATGATACTGACACTTCGTAGATGTAGTTTGACTATTCCTATAC
GTTTCTATCTATTGATGAGGATCCTpoly(A)

FIGURE 5T

SEQ. ID. NO.: 124

>pKVC158

GATTTGGAGAAGCCTTCGCATCAAAACGAGAAGTACGCTCAATTTCTACTCCTCAACTAACCTAGAAT
GACTGCATGGATGCCCCCACCCTACCACACATTTCGAAGAACCTTCCTACGTAAAAGTTAAATAAGAAA
GGAAGGATTGGAACCCCTACAACCTGGTTTCAAGCCAATTTCATAACCATTATGTCTTTCTCAATpoly
(A)

SEQ. ID. NO.: 125

>pKVC160

AAGGATAATGCTGTTTATTAATAATACTCAGGAAGTCAGGGTATTGATGCAATTTTACATACGCACT
TGGGTAGTCTGAAGTTCCATTATTCCAGCAGTTTATATAAATGTTTCAGATCAAAGAGAAAAGAAAACA
CTTTACAGAGACCAGCAGTTGCTTATCAGTTTGGTCATGAGTCTGCTTGTAGTAAAAATAAACTCCCT
CTTGCAATTGCTGAAGAATGTCCTT

SEQ. ID. NO.: 126

>pKVC157

CAGCTCCCTAGTACTTTACTATTATTTCACTAATACTAACAACAAAATAACACACACAAGCACAATAG
ACGCCCCAAGAAGTAGAAACAATTTGAACAATCCTCCAGCTGTCATTCTTATCCTAATTGCCCTTCCCT
CCCTACGAATTCTATACATAATAGACGAGATTAATAACCCAGTTCTAACAGTAAAACTATAGGACACC
AATGATACTGAAGCTATGAATATCTGACTATAAGACCTATGCTTTGACTCCTACATAATCCC

SEQ. ID. NO.: 127

>pKVC156

CCATGCTTGTGACAGACATACAGCCACTTCCAATAAGCAAGCCTCTGCTTCCTGCTACCTGCATGGA
GCCCACTGTGACACTCAGACCATCCCCGGTCACTCACTCGTGTCTGAGAATCTCAGTGAGAGCTGCCTC
TGTCACGGACGGAAGCCAACACAGCCACCTCTCGACCTGGCTCCCCACAGCACCCACCCTCCCTGCATG
CAGCTGTCCCTGCTAACCCCCAATGTTATGTTACACTGTGTAAATCCCCACTGCTGCCGTGTGTGGGTT
GTGTACGTGTCATGTCCTGGTTTATAACTATGGTGCGGTGCGGAAGGATTCTGTAAATGCTGCTCTAA
GA

SEQ. ID. NO.: 128

>pKVC153

CCTAGACTCACAAGTCAAAGTAATACTAATATCTTATTGACCCAATTATTGATCAACGGACCAAGTTAC
CCTAGGGATAACAGCGCAATCCTATTTAAGAGTTCATATCGACAATTAGGGTTTACGACCTCGATGTTG
GATCAGGACATCCAATGGTGCAGAAGCTATTAATGGTTCGTTTGTTCACGATTAAAGTCCTACGTGA
TCTGAGTTCAGACCGGAGCAATCCAGGTCGGTTTCTATCTATTTACAATTTCTCCCAGTACGAAAGGAC
AAGAGAAATGGAGCCTCCTTACCATAAGTGCTCCCAACCAATTTATGpoly(A)

SEQ. ID. NO.: 129

>pKVC152

GCTTCAATTTACTAGTTCAACTTATATAAAAACAACCTAATGGGCTAAAACAAAATAAATATGAACTAA
AAAATTTTCGGTTGGGGTGACCTCGGAGAATAAAAAATCCTCCGAATGATTTTAACCTAGACTCACAAGT
CAAAGTAATACTAATATCTTATTGACCCAATTATTGATCAACGGACCAAGTTACCCTAGGGATAACAGC
GCAATCCTATTTAAGAGTTCATATCGACAATTAGGGCCCACGACCTCGATGTTGGATCAGGACATCCCA
ATGGTGCAGAAGCTATTAATGGTTCGTTTGTTCACGATTAAAGTCCTACGTGATCTGA

FIGURE 5U

SEQ. ID. NO.: 130

>pKVC161

AGAGATATCGGAACCCTCTACCTATTATTTGGAGCCTGAGCAGGAATAGTAGGGACAGCTTTAAGTATT
CTAATTCGAGCTGAAC TAGGACAGCCAGGCGCACTCCTAGGAGATGACCAAATCTATAATGTCATCGTC
ACAGCCCATGCATTGTAATAATTTCTTTATAGTAATACCTATAATAATTGGAGGCTTCGGGAACTGA
CTTGTACCACTAATAATTGGAGCCCCTGATATAGCATTCCCACGAATAAATAACATAAGCTTTTGACTG
CTTCCTCCATCATTTCTACTCC

SEQ. ID. NO.: 131

>pKVC162

GAGCTGTTGCCAGTGTAAGACAGCAAACATGGACACTCTCGCACTGTGCATCACAAAGCTAACAAATC
GAAATCTTGAATGCAGTCTGTCCTAAGTCCAGGCAAGTGACAGCCATGTGTGTCTGCAGTGCTGTGTCA
CCACGTCCTGCATTGTTGGAGCTGCTGCAGGGACACTGAGATGAGCAGGTTCTTTGGAAAGAACTGTTG
TGCTCCTCAAAGCAGTGTTTCAGATTTTAAAGGTTCTTAGCCTCCTCAGTTCCTTATGTGGAAGTGTAGG
ATCCCCTTCATAAATTTTAAAGTGCTTATGTGATCCAATTGGTCTACATTTT

SEQ. ID. NO.: 132

>pKVC36BR

CTTTAGAGAAGGCAGGTCTTACAAACACTACAGAAAAGCCGTTTGGACGTAA
AAATCCAAGGAGAAAGGAGTCATTAGGAAATGTAAACATAGGACACAGAACG
CATGTTGTGTGATGGTCCCTTCTCTCCGTGTGGTTCCAGAATATGCTCCTGAC
CCCAGAGCCGCCACCTGAGCGCGCACCGGGAAGGTCACAGACGACTTCAGGC
TTCAGGCGCAACGTC

WW\MISC-7\2318SEQR\V2

FIGURE 5V

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